

5' NAG GAN GGT GGG GGA CCC ANG GGT CCA GAG CGC AGT TCG GGT CGG AGC TYC GWC
 9 18 27 36 45 54
 CAG GCT GCT GGT ACC TGC GTC CGC CCG GCG AGC AGG ACA GGC TGC TTT GGT TTG
 63 72 81 90 99 108
 TGA CCT CCA GGC AGG ACG GCC ATC CTC TCC AGA ATG AAG ATC TTC TTG CCA GTG
 117 126 135 144 153 162
 M K I F L P V
 CTG CTG GCT GCC CTT CTG GGT GTG GAG CGA GCC 198 207 216
 L L A A L L G V E R A S S L M C F S
 171 180 189 198 207 216
 TGC TTG AAC CAG AAG AGC AAT CTG TAC TGC CTG AAG CCG ACC ATC TGC TCC GAC
 C L N Q K S N L Y C L K P T I C S D
 225 234 243 252 261 270
 CAG GAC AAC TAC TGC CTG ACT GTG TCT GCT AGT GCC GGC ATT GGG AAT CTC GTG
 Q D N Y C V T V S A S A G I G N L V
 279 288 297 306 315 324
 ACA TTT GGC CAC AGC CTG AGC AAG ACC TGT TCC CCG GGC TGC CCC ATC CCA GAA
 T F G H S L S K T C S P A C P I P E
 333 342 351 360 369 378
 GGC GTC AAT GTT GGT GTG GCT TCC ATG GGC ATC AGC TGC TGC CAG AGC TTT CTG
 G V N V G V A S M G I S C C Q S F L
 387 396 405 414 423 432
 TGC AAT TTC AGT GCG GCC GAT GGC GGG CTG CCG GCA AGC GTC ACC CTG CTG GGT
 C N F S A A D G G L R A S V T L L G
 441 450 459 468 477 486
 GCC GGC CTG CTG CTG AGC CTG WTG CCG GGC CTG CTG CCG TTT GGC CCC TGA 3'
 A G L L L S L X P A L L R F G P *

FIGURE 1

5' GTG ACC ATG AAG GCT GTG CTG CTT GCC CTG TTG ATG GCA GGC TTG GCC CTG CAG
 V T M K A V L L A L L M A G L A L Q

CCA GGC ACT GCC CTG CTG TGC TAC TCC TGC AAA GCC CAG GTG AGC AAC GAG GAC
 P G T A L L C Y S C K A Q V S N E D

TGC CTG CAG GTG GAG AAC TGC ACC CAG CTG GGG GAG CAG TGC TGG ACC GCG CGC
 C L Q V E N C T Q L G E Q C W T A R

ATC CGC GCA GTT GGC CTC CTG ACC GTC ATC AGC AAA GCC TGC AGC TTG AAC TGC
 I R A V G L L T V I S K G C S L N C

GTG GAT GAC TCA CAG GAC TAC TAC GTG GGC AAG AAG AAC ATC ACG TGC TGT GAC
 V D D S Q D Y Y V G K K N I T C C D

ACC GAC TTG TGC AAC GSC AGC GGG GCC CAT GCC CTG CAG CCG GCT GCC GCC ATC
 T D L C N X S G A H A L Q P A A A I

CTT GCG CTG CTC CCT GCA CTC GGC CTG CTG CTC TGG GGA CCC GGC CAG CTA TAG
 L A L L P A L G L L L W G P G Q L *

GCT CTG GGG GGC CCC GMT GCA GCC CAC ACT GGG TGT GGT GCC CCA AGG CCT CTG
 A L G G P X A A H T G C G A P R P L

TGS CAC TCC TMA CAG ACC TGG GCC CAG TGG GAG SCT GTC TCT NGG TTC CTG AGG
 X H S X Q T W A Q W E X V S X F L R

CAC ATC CT 3'
 H I

FIGURE 2

1	M	-	-	-	-	-	K	I	F	L	P	V	L	L	A	A	L	L	G	V	E	R	A	S	S	L	M	C	F	scab-1	
1	M	S	A	T	S	N	M	R	V	F	L	P	V	L	L	A	A	L	L	G	M	E	Q	V	H	S	L	M	C	E	GI 434660
1	M	S	T	T	S	S	M	R	V	F	S	I	V	L	Q	A	H	L	L	G	V	E	L	V	P	S	L	I	C	S	GI 1199651
1	M	-	-	-	-	-	K	A	V	L	L	A	L	L	M	A	G	L	A	L	O	P	G	T	A	L	L	C	Y	scab-2	
1	M	-	-	-	-	-	K	A	F	L	F	A	V	L	A	A	V	L	C	V	E	R	A	H	T	L	I	C	F	GI 509840	
25	S	C	L	N	Q	K	S	N	L	Y	C	L	K	P	T	I	C	S	D	Q	D	N	Y	C	V	T	V	S	A	S	scab-1
31	S	C	T	D	Q	K	N	N	I	N	C	L	W	P	V	S	C	Q	E	K	D	H	Y	C	I	T	L	S	A	A	GI 434660
31	S	C	T	H	Q	K	S	N	I	N	P	P	W	P	V	A	C	K	D	T	G	N	Y	C	I	M	L	F	S	A	GI 1199651
25	S	C	K	A	Q	V	S	N	E	D	C	L	Q	V	E	N	C	T	Q	L	G	E	Q	C	W	T	A	R	I	R	scab-2
25	S	C	S	D	A	S	S	N	W	A	C	L	T	P	V	K	C	A	E	N	E	E	H	C	V	T	T	Y	V	G	GI 509840
55	A	G	I	G	N	L	V	T	F	G	H	S	L	S	K	T	C	S	P	A	C	P	I	P	E	-	G	V	N	V	scab-1
61	A	G	F	G	N	-	V	N	L	G	Y	T	L	N	K	G	C	S	P	I	C	P	S	E	N	V	N	L	N	L	GI 434660
61	V	G	F	G	N	-	V	N	L	G	Y	T	L	N	T	G	C	S	Q	S	C	P	H	E	N	I	N	I	N	P	GI 1199651
55	A	V	-	-	G	L	L	T	V	-	-	-	I	S	K	G	C	S	L	N	C	V	D	D	S	O	D	V	V	scab-2	
55	V	G	I	G	G	-	-	K	S	G	Q	S	I	S	K	G	C	S	P	V	C	P	S	A	G	I	N	L	-	-	GI 509840
84	G	V	A	S	M	G	I	S	C	C	Q	S	F	L	C	N	F	S	A	A	D	G	G	L	R	A	S	V	T	L	scab-1
90	G	V	A	S	V	N	S	Y	C	C	O	S	S	F	C	N	F	S	A	A	G	L	G	L	R	A	S	I	P	L	GI 434660
90	G	V	A	S	V	N	S	Y	-	-	O	S	S	F	C	N	F	S	N	A	C	L								GI 1199651	
80	G	K	K	N	I	T	-	-	C	C	D	T	D	L	C	N	X	S	G	A	H	-	A	L	Q	P	A	A	A	I	scab-2
81	G	I	A	A	A	S	V	Y	C	C	D	S	F	L	C	N	I	S	G	S	S	-	S	V	K	A	S	Y	A	V	GI 509840
114	L	G	A	G	L	L	L	S	L	X	P	A	L	L	R	F	G	P													scab-1
120	L	G	L	G	L	L	L	S	L	L	-	A	L	L	Q	L	S	P													GI 434660
109																														GI 1199651	
107	L	A	-	-	-	L	L	P	A	L	G	L	L	L	W	G	P	G	Q	L											scab-2
110	L	A	L	G	I	L	V	S	F	V	-	Y	V	L	R	A	R	E													GI 509840

Decoration 'Decoration #1': Box residues that match the Consensus exactly.

FIGURE 3

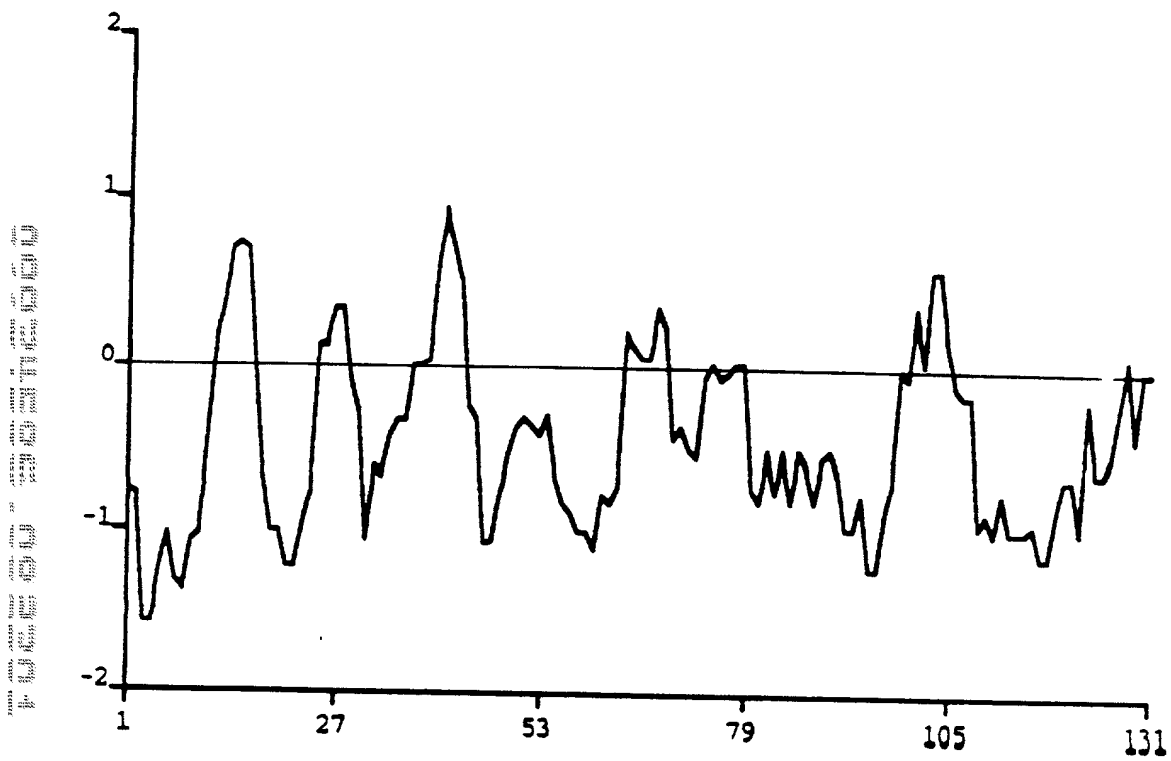


FIGURE 4

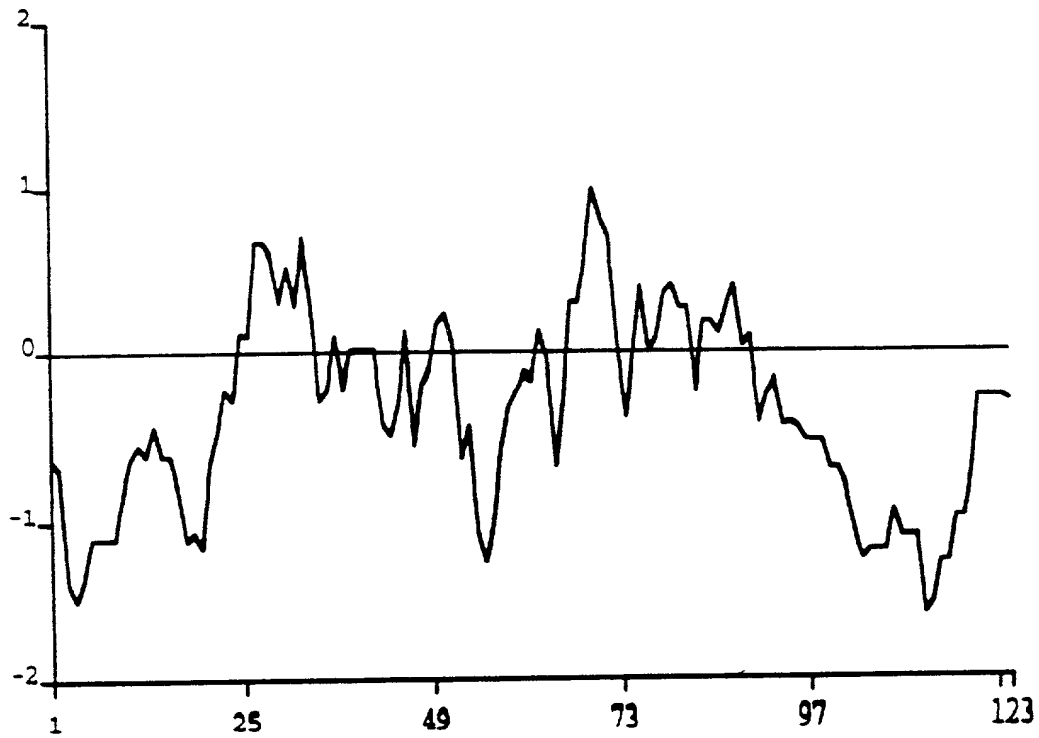


FIGURE 5

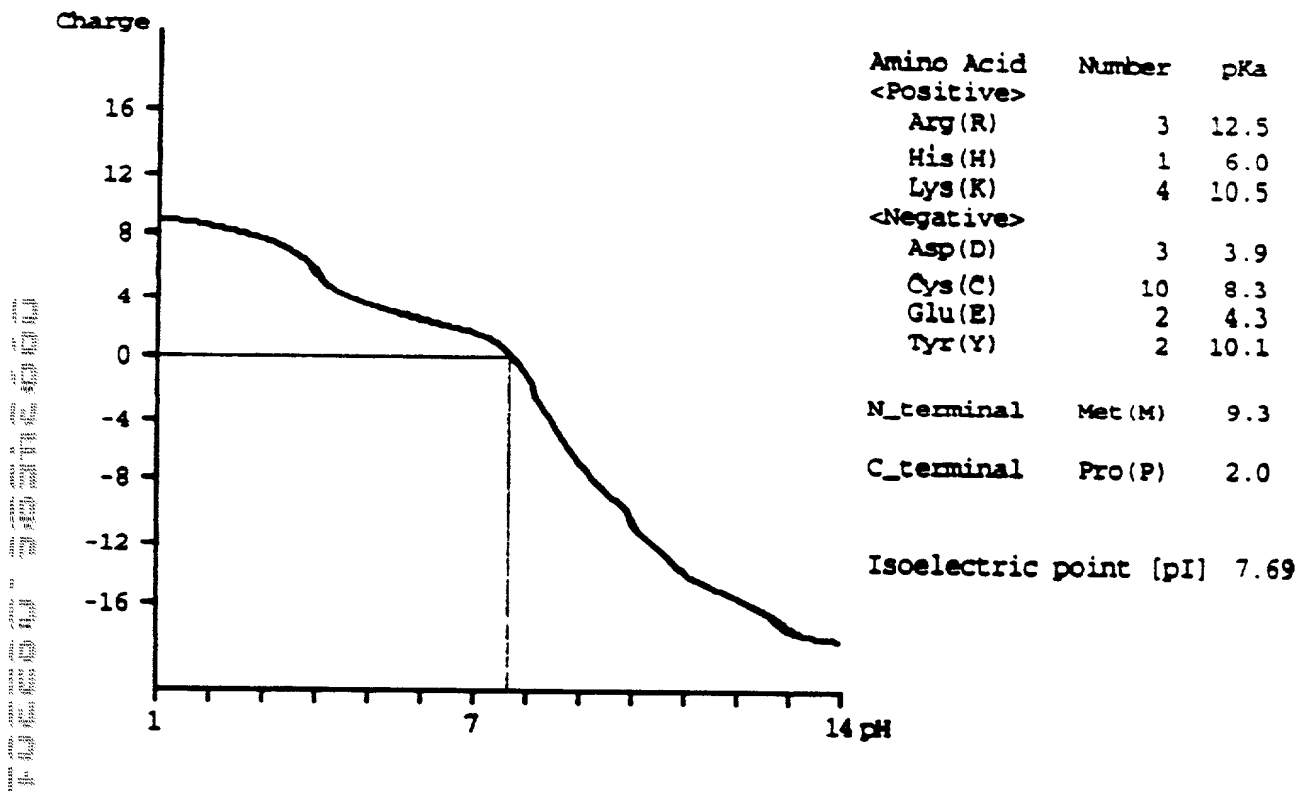
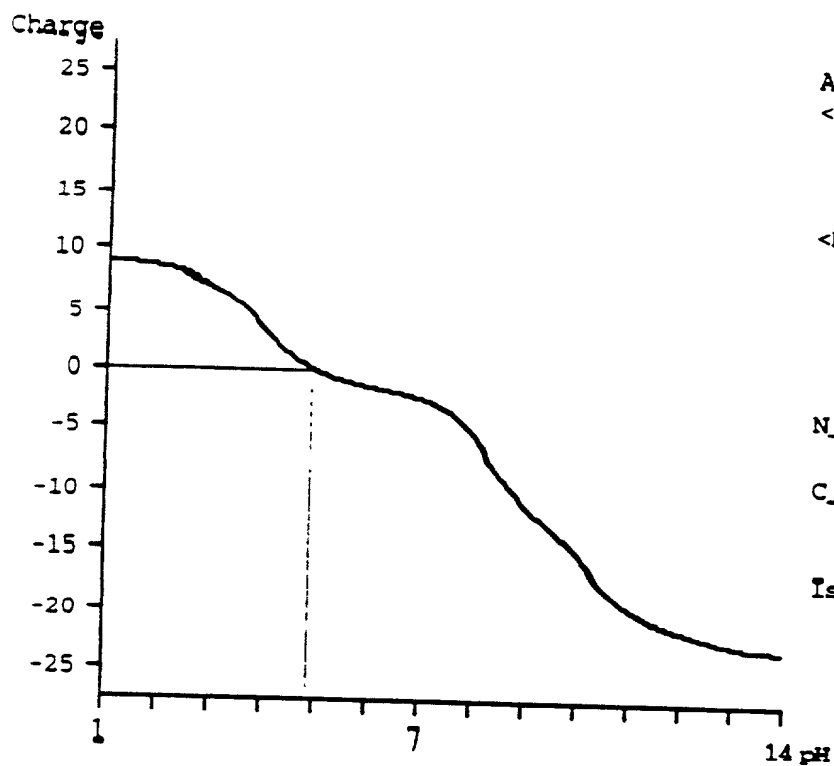


FIGURE 6



Amino Acid	Number	pKa
<Positive>		
Arg (R)	2	12.5
His (H)	1	6.0
Lys (K)	5	10.5
<Negative>		
Asp (D)	6	3.9
Cys (C)	10	8.3
Glu (E)	3	4.3
Tyr (Y)	3	10.1

N_terminal Met (M) 9.3

C_terminal Leu (L) 2.3

Isoelectric point [pI] 4.93

FIGURE 7